

```

10      30      50
-88  GTTGTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29

70      90      110
-28  CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGCTCGCTCCACGCTCT 31
      M A W L G A S L H V W 11
-8

130     150     170
32  GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGCGCCAGAGCCCGAGCTGGATTCTGATGGCA 91
12  G W L M L G S C L L A R A Q L D S D G T 31

190     210     230
92  CCATCACTATAGAGGAGCAGATTGTCTCTGTGCTGAAAGCGAAAGTACAATGTGAAGTCA 151
32  I T I E E Q I V L V L K A K V Q C E L N 51

250     270     290
152 ACATCACAGCTCAACTCCAGGAGGGAGAGGTAATTGTTTCCCTGAATGGGATGGAGTCA 211
52  I T A Q L Q E G E G N C F P E W D G L I 71

310     330     350
212 TTTGTTGGCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATT 271
72  C W P R G T V G K I S A V P C P Y I Y 91

370     390     410
272 ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAACCCCAATGGAACATGGGATT 331
92  D F N H K G V A F R H C N P N G T W D F 111

```

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

332	TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTCTGCAGC	430	450	470	391
112	M H S L N K T W A N Y S D C L R F L Q P				131
392	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCCTCTATGTAATGIATACCGTTG	490	510	530	451
132	D I S I G K Q E F C E R L Y V M Y T V G				151
452	GCTACTCCATCTCTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGAC	550	570	590	511
152	Y S I S F G S L A V A I L I I G Y F R R				171
512	GATTGCATTGCACACTAGGAACATATCCACATGCACCTTATTTGTCTTTCATGCTGAGAG	610	630	650	571
172	L H C T R N Y I H M H L F V S F M L R A				191
572	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG	670	690	710	631
192	T S I F V K D R V V H A H I G V K E L E				211
632	AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT	730	750	770	691
212	S L I M Q D D P Q N S I E A T S V D K S				231
790		810	830		

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

692	CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTACTTTCCTGGCTACAAATT	751
232	Q Y I G C K I A V V M F I Y F L A T N Y	251
	850	870
752	ATTATTGGATCCTGGTGGAAAGGTCCTACCTGCATAATCTCATCTTTGTGGCTTCTTTT	811
252	Y W I L V E G L Y L H N L I F V A F F S	271
	910	930
812	CGGACACCAAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG	871
272	D T K Y L W G F I L I G W G F P A A F V	291
	970	1010
872	TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG	931
292	A A W A V A R A T L A D A R C W E L S A	311
	1030	1070
932	CTGGAGACATCAAGTGGATTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA	991
312	G D I K W I Y Q A P I L A A I G L N F I	331
	1090	1130
992	TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG	1051
332	L F L N T V R V L A T K I W E T N A V G	351
	1150	1190
1052	GGCATGACACAAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCTGTCTCTAG	1111
352	H D T R K Q Y R K L A K S T L V L V L V	371

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

1112	1210	1230	1250	1171
372	TCITGGAGTGCATTACATCGTGTTCGTGCGCTGCCTCACTCCTTCACTGGGCTCGGGT			391
	F G V H Y I V F V C L P H S F T G L G W			
1172	1270	1290	1310	1231
392	GGGAGATCCGCATGCACCTGTGAGCTCTTCTTCAACTCCTTTTCAGGGTTTCTTTGTGCTCA			411
	E I R M H C E L F F N S F Q G F F V S I			
1232	1330	1350	1370	1291
412	TCACTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			431
	I Y C Y C N G E V Q A E V K K M W S R W			
1292	1390	1410	1430	1351
432	GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAG			451
	N L S V D W K R T P P C G S R R C G S V			
1352	1450	1470	1490	1411
452	TGCTCACCACCGTGACGCACAGCACAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT			471
	L T T V T H S T S S Q S Q V A A A H A W			
1412	1510	1530	1550	1471
472	GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC			491
	C L S L A K L P R S P A D S L T A T S L			

MATCH WITH FIG. 1E

FIG.1D

MATCH WITH FIG. 1D

1472	TTTTACCTGGCTATGCTGGAGTA	1570	1590	1610	1531
492	Y L A M S G V T Q S R T A S H T L S T R				511
1532	GGAGCAACAAGGAAGATAGTGGGAGGAGAGATGATATTCTAATGGAGAAGCCTTCCA	1630	1650	1670	1591
512	S N K E D S G R Q R D D I L M E K P S R				531
1592	GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT	1690	1710	1730	1651
532	P M E S N P D T E G				541
1652	GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAAATGGCTGTTGTGTGAGAGGGC	1750	1770	1790	1711
1712	TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA	1810	1830	1850	1771
1772	TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG	1870	1890	1910	1831
1832	TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT	1930	1950	1970	1891
1892	GGTATTGCTCTGTGATTGTTCA	1990			1914

FIG. 1E

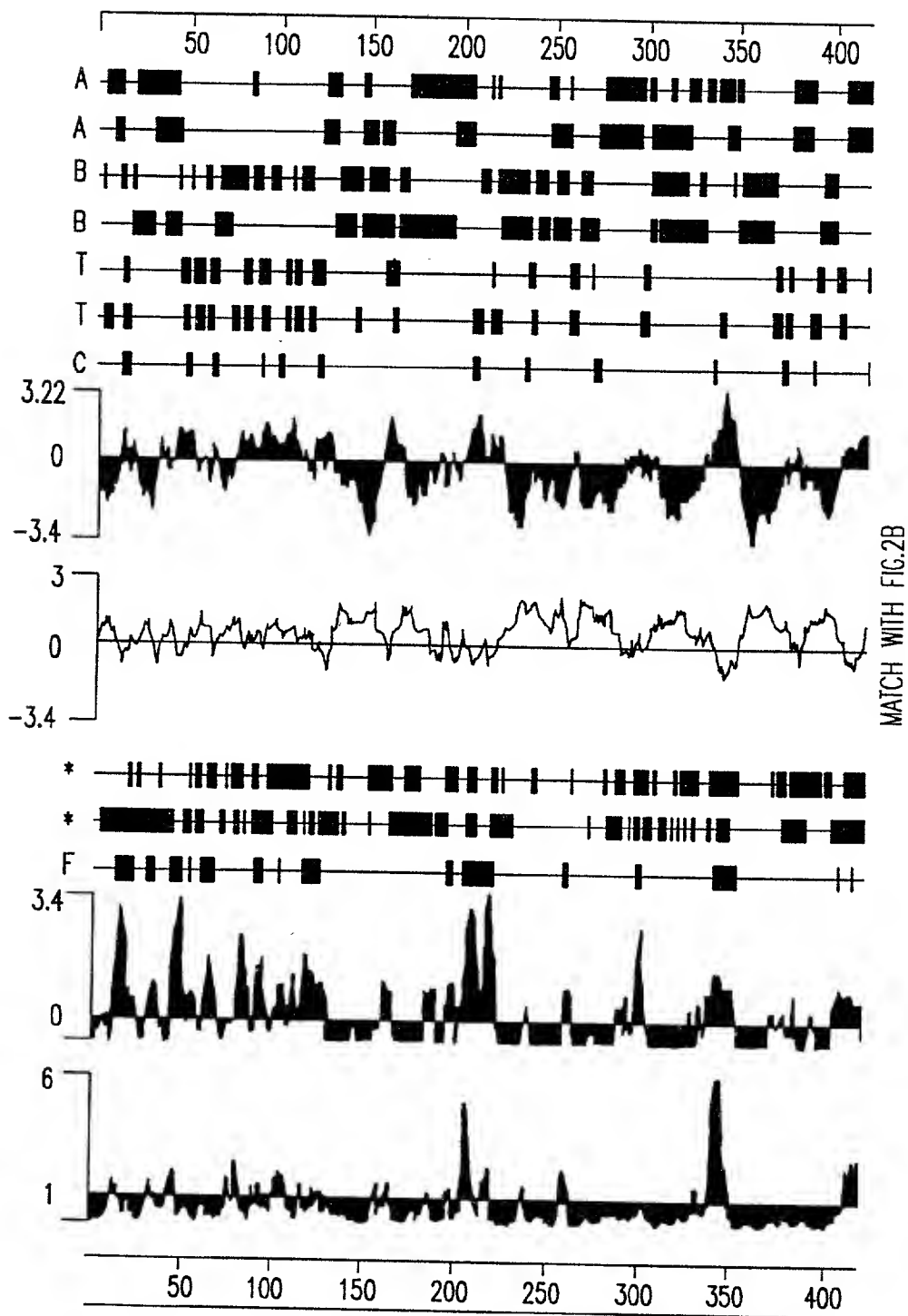


FIG. 2A

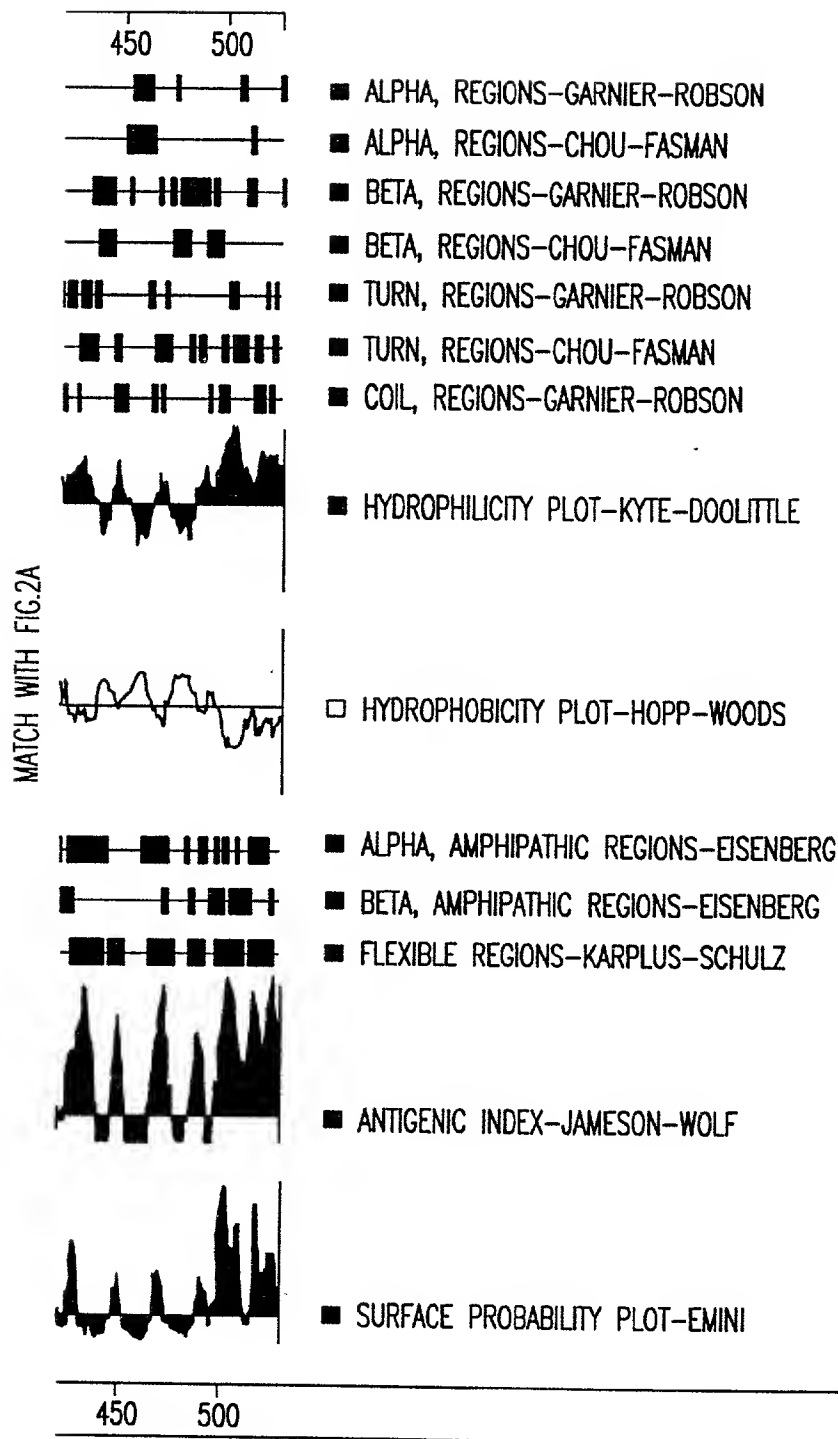


FIG. 2B

# TABLE 6A53A60

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Probability P(N)	N
gp M74445 OPOPTH_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroid...	+3	597	2.9e-203	6
gp L04308 HUMPTH_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189	5
gp M77184 RATPATHR_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188	5
gp X78936 MPHPR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188	5
gp L34611 MUSPTH06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH\_1 parathyroid hormone receptor [Didelphis virginiana]  
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG.3A



Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFYFLATNYWILVEGLYHNLIFVAFFSDT 908  
 I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+  
 Sbjct: 253 ITEEELRAFTPEPPADKAGFVGCRAVTVFLYFLT TNYWILVEGLYHLSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWFPAAFAA VARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF 1088  
 KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF  
 Sbjct: 313 KYLWGF TLFGWGLPAVFVAVVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372

Query: 1089 LNTVRVLATKIWEITNAVGHDTRKQYRKLAKSTLVLVFGVHYIVFVCLPHS 1244  
 +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++  
 Sbjct: 373 INIIRVLATKLRETNAGRC DTRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTW 446  
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKG A+R C+ NG+W+ + N+TW  
 Sbjct: 102 DGFCLPEWDNIWCWPAGVPGKVAVPCPYIYDFNHHKGRAYRRCDSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476  
 ANYS+C++FL  
 Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLVMTYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHHLFVSFMLRATSIFV 677  
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHHLFVSFMLRA SIF+  
 Match with FIG. 3 C

FIG.3B

MATCH WITH FIG. 3B

177 EREVFDRLGMIYTVGYISISGLSTVAVLILGYFRRLLHCTRNYYTHMHLFVSFMLRAVSIFI 236

Sbjct:

678 KDRVVHAHIGVKELESIMQD 740

Query:

KD V+++ + E+E + ++

Sbjct:

237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204

Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSFQGFVSIYYCNCNGEVQAEVKKMWSRWNLSDWKRTPPCGS 1424

Sbjct:

+G+ W+++MH E+ FNSFQGFV+IYC+CNGEVQAE+KK WSRW L++D+KR GS 485

Sbjct:

427 SGILWQVQMHYEMLFNSFQGFVAIYYCNCNGEVQAEIKKSWSRWTLALDFKRRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204

Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query:

159 AQLDSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct:

24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204

Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query:

1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct:

512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C